

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/551,655
Source: P5/10
Date Processed by STIC: 10/14/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

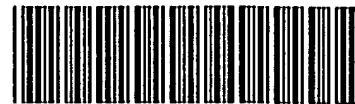
TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



*Suggestion: Consult
Sequence Rules for valid format.*

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/551,655

DATE: 10/14/2005
TIME: 13:33:03

Input Set : N:\RJAVED\10551655.txt
Output Set: N:\CRF4\10142005\J551655.raw

3 <110> APPLICANT: Nihon university
W--> 4 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE
W--> 5 DEHYDRATASE AND USE THEREOF
W--> 6 <130> FILE REFERENCE: 10465
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/551,655
C--> 7 <141> CURRENT FILING DATE: 2005-09-28
7 <150> PRIOR APPLICATION NUMBER: JP 2003-092337
W--> 8 <151> PRIOR FILING DATE: (2003-3-28) 2003-03-28
W--> 9 <160> NUMBER OF SEQ ID: 10

pg 1-3
**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES

replace with
251 <210> SEQ ID NO: 4
252 <211> LENGTH: 19 *960*
E--> 253 <212> TYPE: ~~260~~ *move "DNA" to <212> response*
254 <213> ORGANISM: Glycine max
delete 2237 255 <223> OTHER INFORMATION: *DNA*
E--> 257 <400> SEQUENCE: 4
258 atg gcg aag gag ata gtg aaa gag ctt ctt cct cta att cga gtg tac 48
259 Met Ala Lys Glu Ile Val Lys Glu Leu Leu Pro Leu Ile Arg Val Tyr
260 1 5 10 15
262 aag gat ggc agc gtg gag cgt ctt cta agc tct gaa aac gtg gca gcc 96
263 Lys Asp Gly Ser Val Glu Arg Leu Leu Ser Ser Glu Asn Val Ala Ala
264 20 25 30
266 tcc cct gaa gat ccc caa act gga gtc tca tcc aaa gac ata gtc atc 144
267 Ser Pro Glu Asp Pro Gln Thr Gly Val Ser Ser Lys Asp Ile Val Ile
268 35 40 45
270 gca gac aac ccc tac gtc tcc gct cgc att ttc ctt ccc aaa tcc cac 192
271 Ala Asp Asn Pro Tyr Val Ser Ala Arg Ile Phe Leu Pro Lys Ser His
272 50 55 60
274 cac act aac aac aaa ctc ccc atc ttc ctc tac ttc cac ggt ggc gcc 240
275 His Thr Asn Asn Lys Leu Pro Ile Phe Leu Tyr Phe His Gly Gly Ala
276 65 70 75 80
278 ttt tgc gtc gaa tcc gcc ttc tcc ttt ttc gtc cac cgc tat ctc aac 288
279 Phe Cys Val Glu Ser Ala Phe Ser Phe Phe Val His Arg Tyr Leu Asn
280 85 90 95
282 atc ttg gcc tca gaa gcc aac ata ata gcc atc tcc gtc gac ttc aga 336
283 Ile Leu Ala Ser Glu Ala Asn Ile Ile Ala Ile Ser Val Asp Phe Arg
284 100 105 110
286 ctc ctc cca cac cac cct atc cct gct gcc tac gaa gac ggt tgg acc 384
287 Leu Leu Pro His His Pro Ile Pro Ala Ala Tyr Glu Asp Gly Trp Thr
288 115 120 125

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```

290 acc ctc aaa tgg att gct tcc cac gcc aac aac acc aac acc acc aac      432
291 Thr Leu Lys Trp Ile Ala Ser His Ala Asn Asn Thr Asn Thr Thr Asn
292      130                      135                      140
294 ccg gag cca tgg cta ctc aac cac gcc gac ttc acc aaa gtc tac gta      480
295 Pro Glu Pro Trp Leu Leu Asn His Ala Asp Phe Thr Lys Val Tyr Val
296 145                      150                      155                      160
298 gga ggt gaa acc agc ggt gct aac atc gca cac aac ctg ctt ttg cgt      528
299 Gly Gly Glu Thr Ser Gly Ala Asn Ile Ala His Asn Leu Leu Leu Arg
300      165                      170                      175
302 gca ggt aac gaa tcc ctc ccc ggg gat ctg aaa ata ttg ggt gga tta      576
303 Ala Gly Asn Glu Ser Leu Pro Gly Asp Leu Lys Ile Leu Gly Gly Leu
304      180                      185                      190
306 cta tgc tgc ccc ttc ttc tgg ggc tgc aag cca att ggg tgc gag gct      624
307 Leu Cys Cys Pro Phe Phe Trp Gly Ser Lys Pro Ile Gly Ser Glu Ala
308      195                      200                      205
310 gtt gag ggg cac gag cag agt ttg gcc atg aag gtc tgg aac ttt gcc      672
311 Val Glu Gly His Glu Gln Ser Leu Ala Met Lys Val Trp Asn Phe Ala
312      210                      215                      220
314 tgc cct gat gcc ccc ggt gga atc gat aac ccc tgg atc aac ccc tgt      720
315 Cys Pro Asp Ala Pro Gly Gly Ile Asp Asn Pro Trp Ile Asn Pro Cys
316 225                      230                      235                      240
318 gtt cct ggg gca ccc tct ttg gcc act ctt gcc tgc tct aag ttg ctc      768
319 Val Pro Gly Ala Pro Ser Leu Ala Thr Leu Ala Cys Ser Lys Leu Leu
320      245                      250                      255
322 gtt act atc act ggc aaa gac gag ttc aga gac aga gat att ctc tac      816
323 Val Thr Ile Thr Gly Lys Asp Glu Phe Arg Asp Arg Asp Ile Leu Tyr
324      260                      265                      270
326 cac cac acc gtt gag caa agt ggc tgg caa ggt gaa ctt caa ctc ttt      864
327 His His Thr Val Glu Gln Ser Gly Trp Gln Gly Glu Leu Gln Leu Phe
328      275                      280                      285
330 gat gct ggc gat gag gag cat gct ttc cag ctc ttc aag cct gag act      912
331 Asp Ala Gly Asp Glu Glu His Ala Phe Gln Leu Phe Lys Pro Glu Thr
332      290                      295                      300
334 cat ctt gct aaa gcc atg atc aaa cgc ttg gct tct ttt ctg gtt tga      960
335 His Leu Ala Lys Ala Met Ile Lys Arg Leu Ala Ser Phe Leu Val
336 305                      310                      315
383 <210> SEQ ID NO: 10
384 <211> LENGTH: 30
385 <212> TYPE: DNA
386 <213> ORGANISM: Artificial Sequence
W--> 388 <220> FEATURE:
W--> 388 <223> OTHER INFORMATION:
W--> 388 <400> 10
389 gggagctcga gtcaaaccag aaaagaagcc 30
E--> 394 1/14

```

Delete

Explanation needed
for "Artificial Sequence"
(see p.3)

this error appears
in other sequences
(see p.3)

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/551,655

DATE: 10/14/2005
TIME: 13:33:04

Input Set : N:\RJAVED\10551655.txt

Output Set: N:\CRF4\10142005\J551655.raw

error explanation
Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:5,6,7,8,9,10

VERIFICATION SUMMARY

DATE: 10/14/2005

PATENT APPLICATION: US/10/551,655

TIME: 13:33:04

Input Set : N:\RJAVED\10551655.txt

Output Set: N:\CRF4\10142005\J551655.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:16 M:283 W: Missing Blank Line separator, <220> field identifier
L:253 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:4
L:257 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
L:344 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:344 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:344 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:344
L:353 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:353 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:353 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:353
L:361 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:361 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:361 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:361
L:370 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:370 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:370 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:370
L:379 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:379 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:379 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:379
L:388 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:388 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:388 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:388
L:394 M:254 E: No. of Bases conflict, LENGTH:Input:14 Counted:31 SEQ:10
L:394 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:394 M:252 E: No. of Seq. differs, <211> LENGTH:Input:30 Found:31 SEQ:10